The I.M.A.G.E. Consortium Mouse Gene Project.

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The I.M.A.G.E. Consortium was founded in 1993 to accelerate gene discovery through the use of arrayed gene libraries, and to aid in the accumulation of sequence, map, and expression information for all genes through an Integrated Molecular Analysis of Genomes and their Expression. Directionally cloned, oligo (dT)-primed plasmid cDNA libraries are obtained from several commercial and private sources, with the majority of libraries being normalized libraries made by Dr. M. Bento Soares (Columbia Univ). Following the model initially established with human cDNAs, mouse cDNA clones are arrayed and assigned unique I.M.A.G.E. and MGI accession numbers at LLNL, and then sequenced and sized thanks to the Genome Sequencing Center at Washington University with support from the Howard Hughes Medical Institute. All suitable mouse sequences are annotated and deposited immediately into the NCBI dbEST database (40,000+ so far). Over 1,000 laboratories worldwide have already received (human or mouse) royalty-free I.M.A.G.E. clones from a network of five distributors and have agreed to submit additional sequence, mapping, and expression data to public databases.

We will report on four aspects of the project: (i) the need to obtain mouse cDNA libraries representing diverse tissues and times of development, (ii) efforts to maximize the efficiency of finding the remaining undiscovered genes, (iii) improved WWW-based access to integrated views of sequence, map, and expression information for each gene, and (iv) the master re-arrays being generated to provide a convenient (one clone, one gene) array for large-scale expression and mapping (in particular, to BAC arrays) studies. Further information about the I.M.A.G.E. Consortium is available by email (info@image.llnl.gov) or through the WWW URL:http://www-bio.llnl.gov/bbrp/image/image.html/.